```
          10        20        30        40        50        60        70        80        90
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890
ATGGCTTTGG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA AATGAATGGC ACTTATGACT ACAGTCAATA TGAACTGATC   90
M  A  L  E  Q  N  Q  S  T  D  Y  Y  Y  E  E  N  E  M  N  G  T  Y  D  Y  S  Q  Y  E  L  I

TGTATCAAAG AAGATGTCAG AGAATTTGCA AAAGTTTTCC TCCCTGTATT CCTCACAATA GTTTTCGTCA TTGGACTTGC AGGCAATTCC  180
C  I  K  E  D  V  R  E  F  A  K  V  F  L  P  V  F  L  T  I  V  F  V  I  G  L  A  G  N  S

ATGGTAGTGG CAATTTATGC CTATTACAAG AAACAGAGAA CCAAAACAGA TGTGTACATC CTGAATTTGG CTGTAGCAGA TTTACTCCTT  270
M  V  V  A  I  Y  A  Y  Y  K  K  Q  R  T  K  T  D  V  Y  I  L  N  L  A  V  A  D  L  L  L

CTATTCACTC TGCCTTTTTG GCTGTTAAT GCAGTTCATG GGTGGGTTTT AGGGAAAATA ATGTGCAAAA TAACTTCAGC CTTGTACACA  360
L  F  T  L  P  F  W  A  V  N  A  V  H  G  W  V  L  G  K  I  M  C  K  I  T  S  A  L  Y  T

CTAAACTTTG TCTCTGGAAT GCAGTTTCTG GCTTGTATCA GCATAGACAG ATATGTGGCA GTAACTAAAG TCCCCAGCCA ATCAGGAGTG  450
L  N  F  V  S  G  M  Q  F  L  A  C  I  S  I  D  R  Y  V  A  V  T  K  V  P  S  Q  S  G  V

GGAAAACCAT GCTGGATCAT CTGTTTCTGT GTCTGGATGG CTGCCATCTT GCTGAGCATA CCCCAGCTGG TTTTTTATAC AGTAAATGAC  540
G  K  P  C  W  I  I  C  F  C  V  W  M  A  A  I  L  L  S  I  P  Q  L  V  F  Y  T  V  N  D

AATGCTAGGT GCATTCCCAT TTTCCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT CAAATGCTAG AGATCTGCAT TGGATTTGTA  630
N  A  R  C  I  P  I  F  P  R  Y  L  G  T  S  M  K  A  L  I  Q  M  L  E  I  C  I  G  F  V

GTACCCTTTC TTATTATGGG GGTGTGCTAC TTTATCACAG CAAGGACACT CATGAAGATG CCAAACATTA AAATATCTCG ACCCCTAAAA  720
V  P  F  L  I  M  G  V  C  Y  F  I  T  A  R  T  L  M  K  M  P  N  I  K  I  S  R  P  L  K

GTTCTGCTCA CAGTGGTTAT AGTTTTCATT GTCACTCAAC TGCCTTAATA CATTGTCAAG TTCTGCGGAG CCATAGACAT CATCTACTCC  810
V  L  L  T  V  V  I  V  F  I  V  T  Q  L  P  Y  N  I  V  K  F  C  R  A  I  D  I  I  Y  S

CTGATCACCA GCTGCAACAT GAGCAAACGC ATGGACATCG CCATCCAAGT CACAGAAAGC ATCGCACTCT TTCACAGCTG CCTCAACCCA  900
L  I  T  S  C  N  M  S  K  R  M  D  I  A  I  Q  V  T  E  S  I  A  L  F  H  S  C  L  N  P

ATCCTTTATG TTTTTATGGG AGCATCTTTC AAAAACTACG TTATGAAAGT GGCCAAGAAA TATGGGTCCT GGAGAAGACA GAGACAAAGT  990
I  L  Y  V  F  M  G  A  S  F  K  N  Y  V  M  K  V  A  K  K  Y  G  S  W  R  R  Q  R  Q  S

GTGGAGGAGT TTCCTTTTGA TTCTGAGGGT CCTACAGAGC CAACCAGTAC TTTTAGCATT TAAAGGTAAA ACTGCTCTGC CTTTTGCTTG 1080
V  E  E  F  P  F  D  S  E  G  P  T  E  P  T  S  T  F  S  I  .  R  .  N  C  S  A  F  C  L

GATACATATG AATGATGCTT TCCCCTCAAA TAAAACATCT GCCTTATTCT GAAAAAAAAA AAAAAAM                    1147
D  T  Y  E  .  C  F  P  L  K  .  N  I  C  L  I  L  K  K  K  K  K
```

FIG. 1
(SEQ. ID NO: 1 & 2)

A

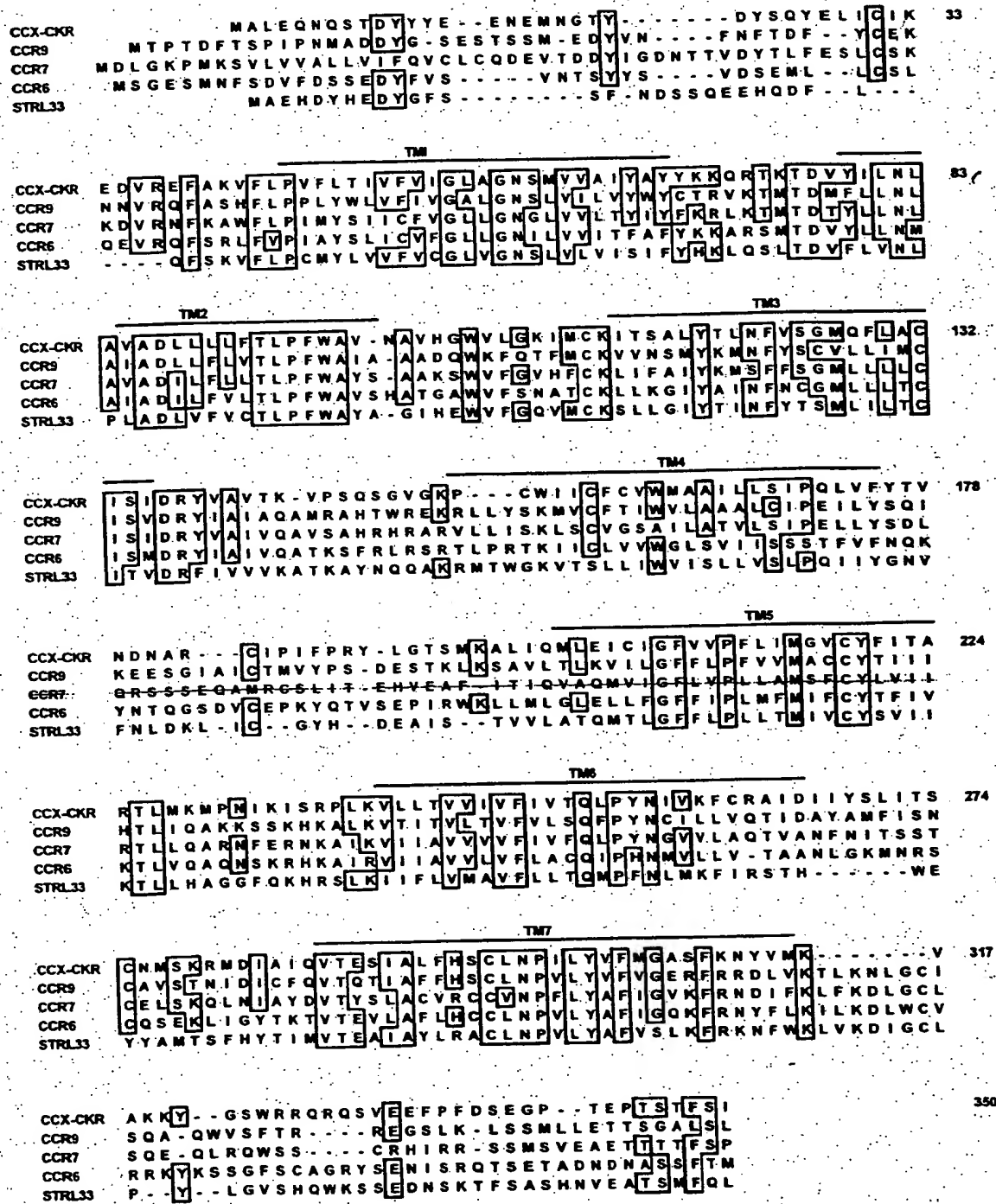

CCX-CKR
CCR9
CCR7
CCR6
STRL33
TM1
TM2
TM3
TM4
TM5
TM6
TM7
33
83
132
178
224
274
317
350

FIG. 2(a)

B

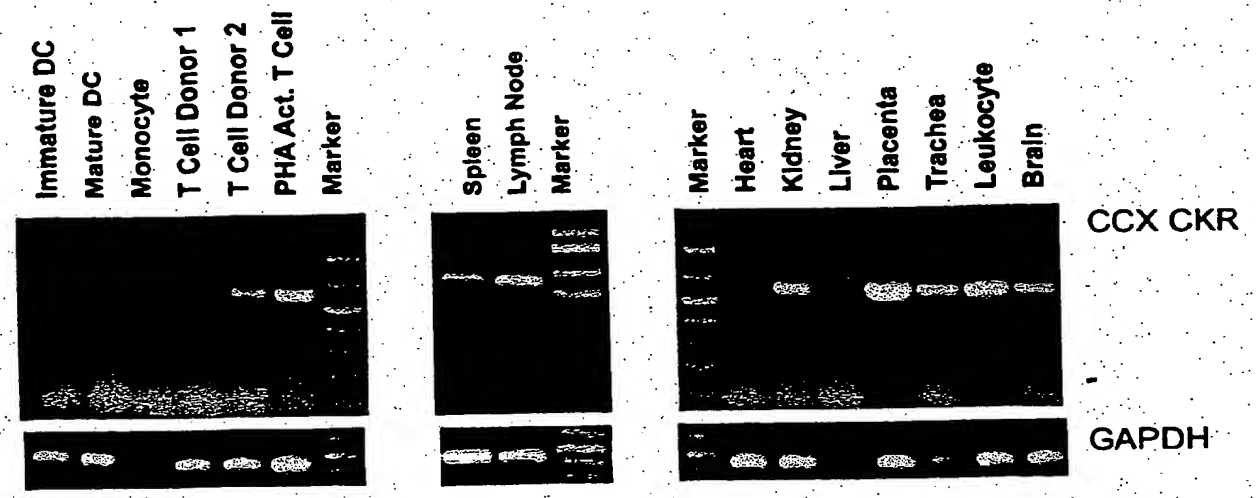


FIG. 2(b)

C

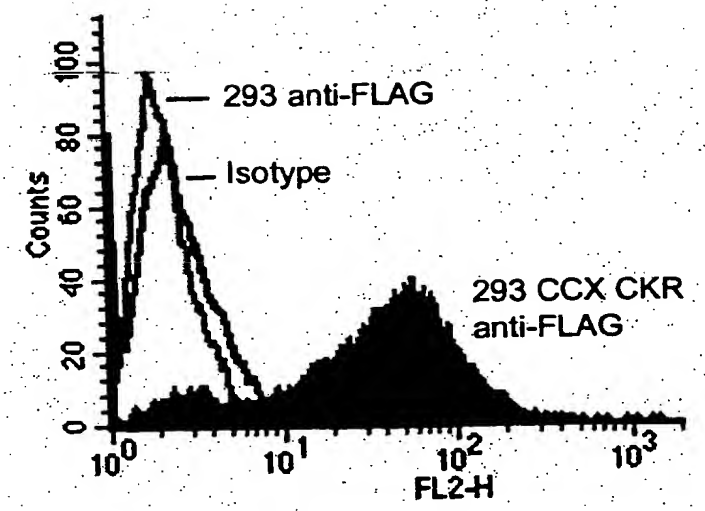
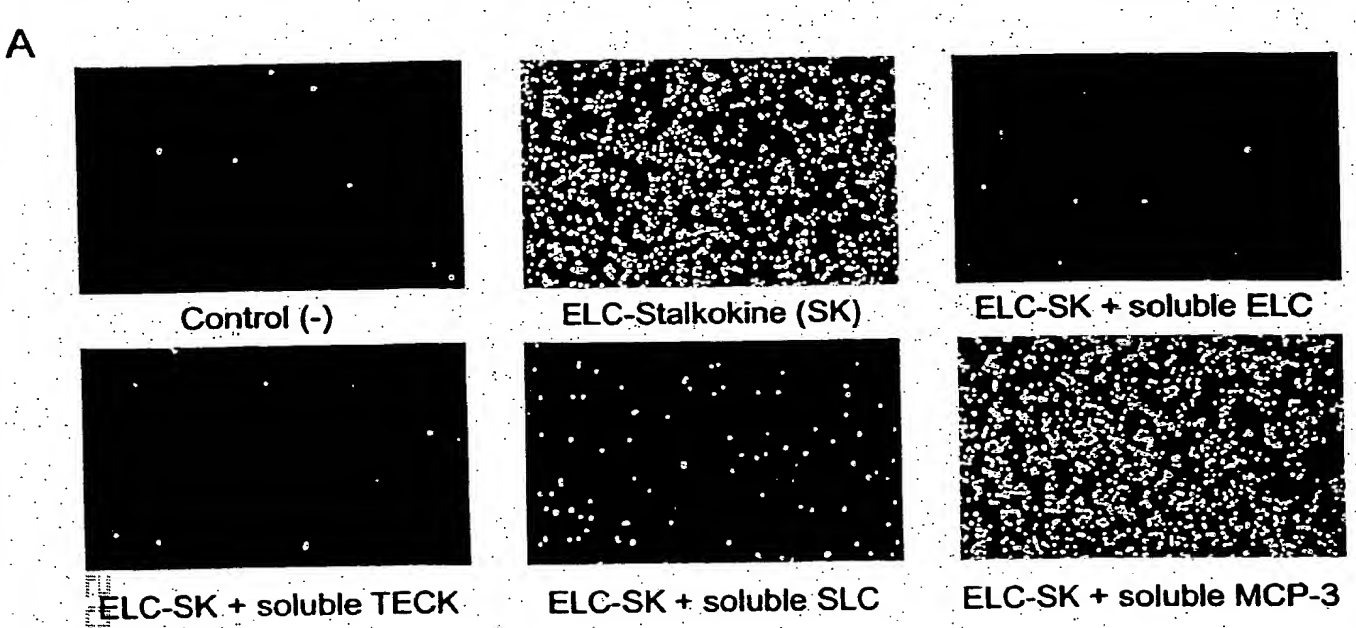


FIG. 2(c)

FIG. 3(a)



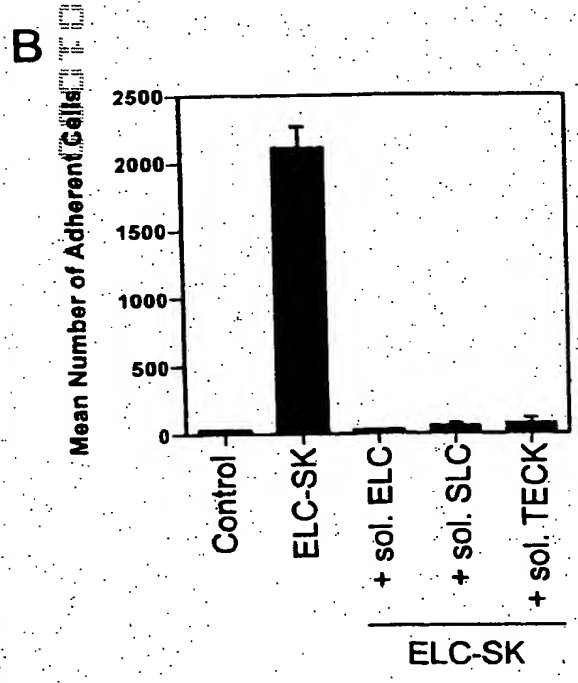


FIG. 3(b)

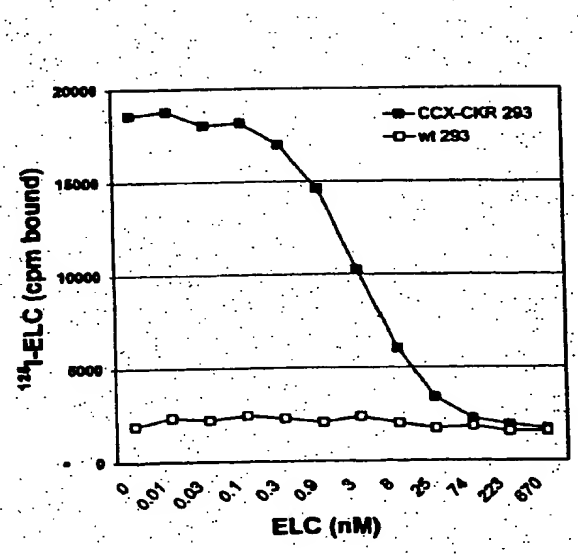


FIG. 3(c)

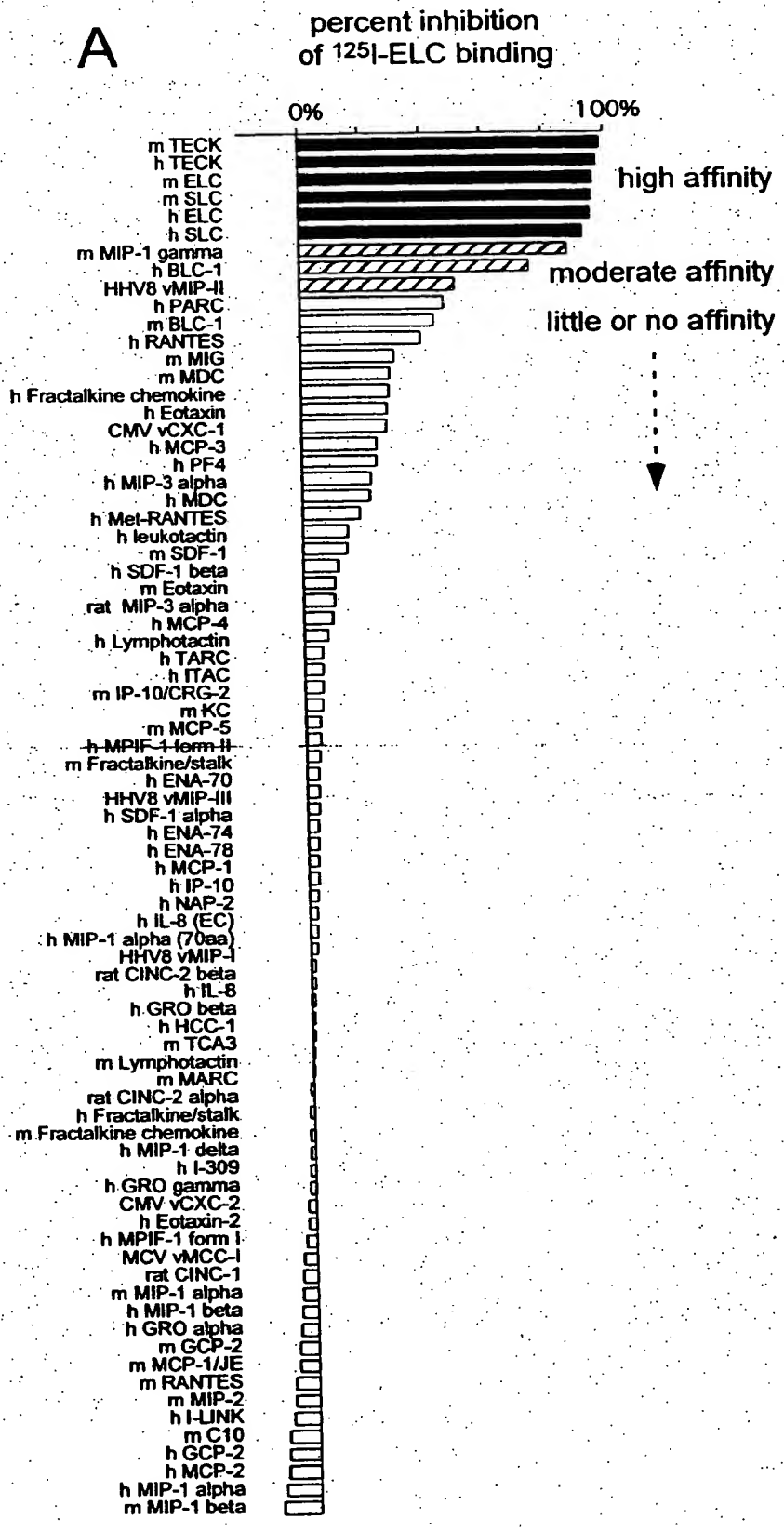
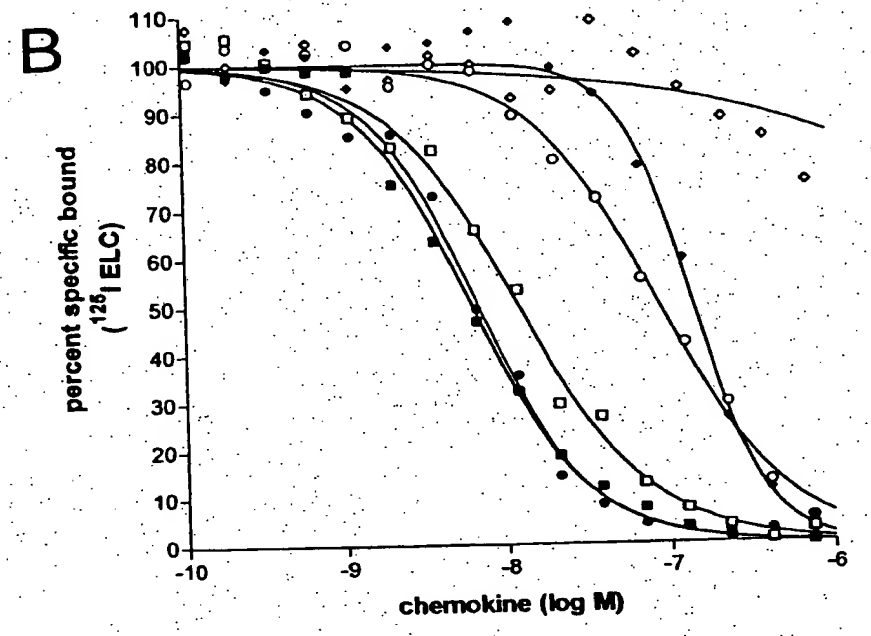

A
percent inhibition
of 125I-ELC binding
0%
100%
high affinity
moderate affinity
little or no affinity
m TECK
h TECK
m ELC
m SLC
h ELC
h SLC
m MIP-1 gamma
h BLC-1
HHV8 vMIP-II
h PARC
m BLC-1
h RANTES
m MIG
m MDC
h Fractalkine chemokine
h Eotaxin
CMV vCXC-1
h MCP-3
h PF4
h MIP-3 alpha
h MDC
h Met-RANTES
h leukotactin
m SDF-1
h SDF-1 beta
m Eotaxin
rat MIP-3 alpha
h MCP-4
h Lymphotactin
h TARC
h ITAC
m IP-10/CRG-2
m KC
m MCP-5
h MPIF-1 form II
m Fractalkine/stalk
h ENA-70
HHV8 vMIP-III
h SDF-1 alpha
h ENA-74
h ENA-78
h MCP-1
h IP-10
h NAP-2
h IL-8 (EC)
h MIP-1 alpha (70aa)
HHV8 vMIP-I
rat CINC-2 beta
h IL-8
h GRO beta
h HCC-1
m TCA3
m Lymphotactin
m MARC
rat CINC-2 alpha
h Fractalkine/stalk
m Fractalkine chemokine
h MIP-1 delta
h I-309
h GRO gamma
CMV vCXC-2
h Eotaxin-2
h MPIF-1 form I
MCV vMCC-I
rat CINC-1
m MIP-1 alpha
h MIP-1 beta
h GRO alpha
m GCP-2
m MCP-1/JE
m RANTES
m MIP-2
h I-LINK
m C10
h GCP-2
h MCP-2
h MIP-1 alpha
m MIP-1 beta

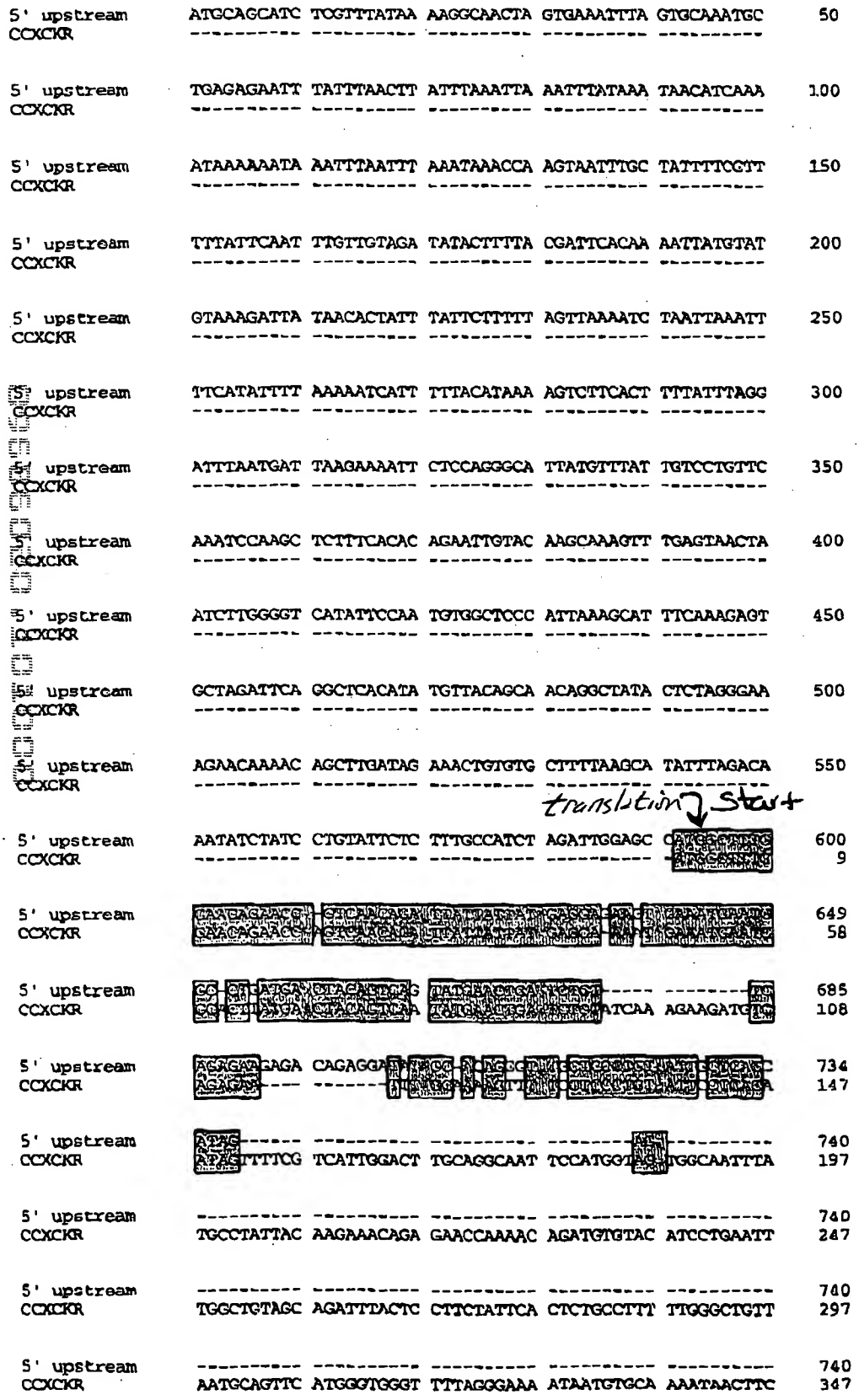
FIG. 4(a)



human chemokines	IC-50	murine chemokines	IC-50
■ h ELC	6 nM	m ELC	1 nM
□ h SLC	12 nM	m SLC	4 nM
● h TECK	7 nM	m TECK	2 nM
◆ h BLC-1	140 nM	m MIP-1γ	70 nM
○ HHV8 vMIP-II	90 nM		
◇ h MCP-3	>2000 nM		

FIG. 4(b)

FIG. 5


5' upstream ATGCAGCATC TCGTTTATAA AAGGCAACTA GTGAAATTTA GTGCAAATGC 50
CCXCKR
5' upstream TGAGAGAATT TATTTAACTT ATTTAAATTA AATTTATAAA TAACATCAAA 100
CCXCKR
5' upstream ATAAAAAATA AATTTAATTT AAATAAACCA AGTAATTTGC TATTTTCGTT 150
CCXCKR
5' upstream TTTATTCAAT TTGTTGTAGA TATACTTTTA CGATTCACAA AATTATGTAT 200
CCXCKR
5' upstream GTAAAGATTA TAACACTATT TATTCTTTTT AGTTAAAATC TAATTAAATT 250
CCXCKR
5' upstream TTCATATTTT AAAAATCATT TTTACATAAA AGTCTTCACT TTTATTTAGG 300
CCXCKR
5' upstream ATTTAATGAT TAAGAAAATT CTCCAGGGCA TTATGTTTAT TGTCCTGTTC 350
CCXCKR
5' upstream AAATCCAAGC TCTTTCACAC AGAATTGTAC AAGCAAAGTT TGAGTAACTA 400
CCXCKR
5' upstream ATCTTGGGGT CATATTCCAA TGTGGCTCCC ATTAAAGCAT TTCAAAGAGT 450
CCXCKR
5' upstream GCTAGATTCA GGCTCACATA TGTTACAGCA ACAGGCTATA CTCTAGGGAA 500
CCXCKR
5' upstream AGAACAAAAC AGCTTGATAG AAACTGTGTG CTTTTAAGCA TATTTAGACA 550
CCXCKR
translation Start
5' upstream AATATCTATC CTGTATTCTC TTTGCCATCT AGATTGGAGC 600
CCXCKR 9
5' upstream 649
CCXCKR 58
5' upstream 685
CCXCKR 108
5' upstream 734
CCXCKR 147
5' upstream 740
CCXCKR TCATTGGACT TGCAGGCAAT TCCATGGT TGGCAATTTA 197
5' upstream 740
CCXCKR TGCCTATTAC AAGAAACAGA GAACCAAAAC AGATGTGTAC ATCCTGAATT 247
5' upstream 740
CCXCKR TGGCTGTAGC AGATTTACTC CTTCTATTCA CTCTGCCTTT TTGGGCTGTT 297
5' upstream 740
CCXCKR AATGCAGTTC ATGGGTGGGT TTTAGGGAAA ATAATGTGCA AAATAACTTC 347

Internalization by FACS 45 minute Incubation

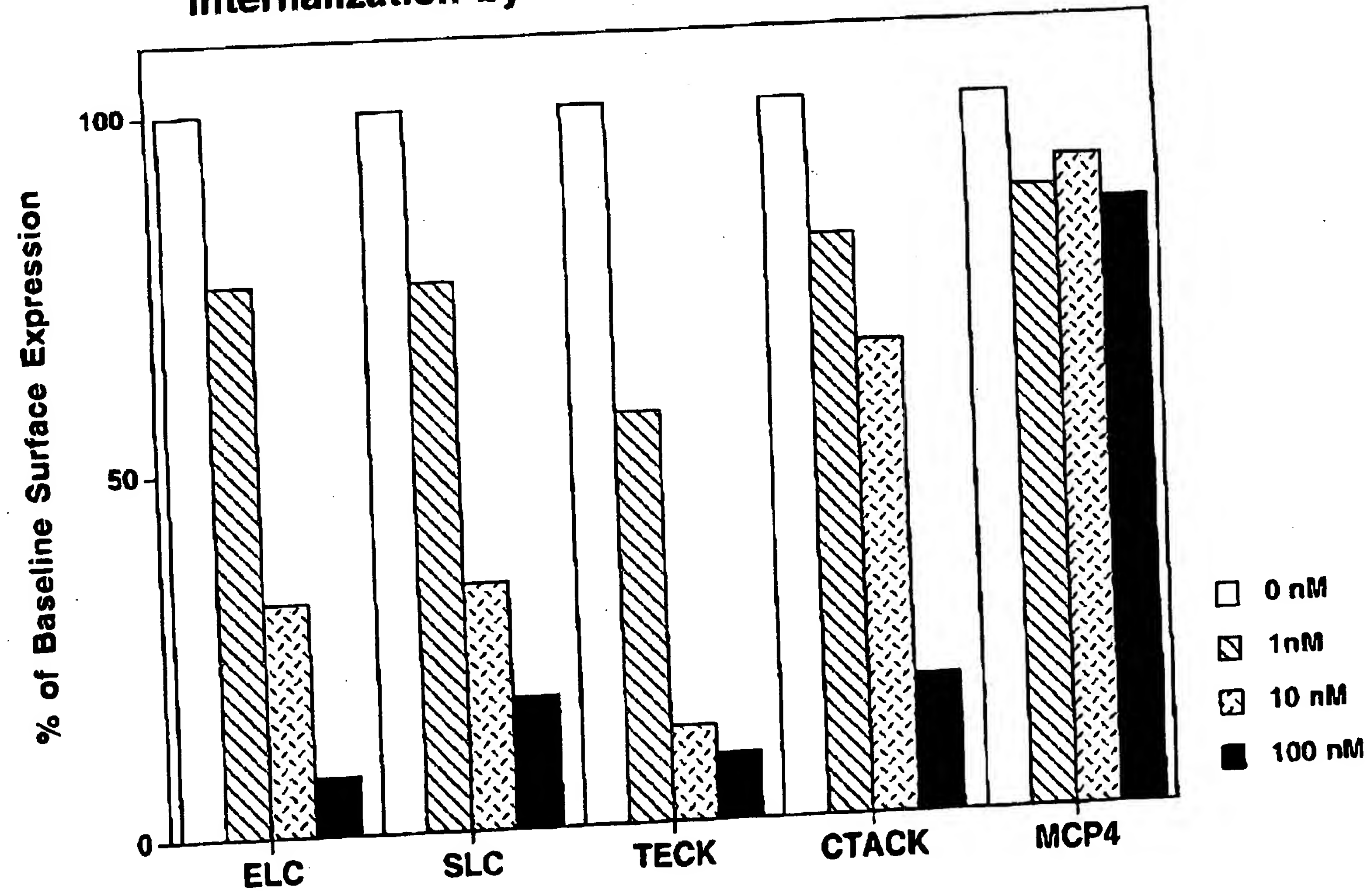


Fig. 6A

000T0T" 02098960

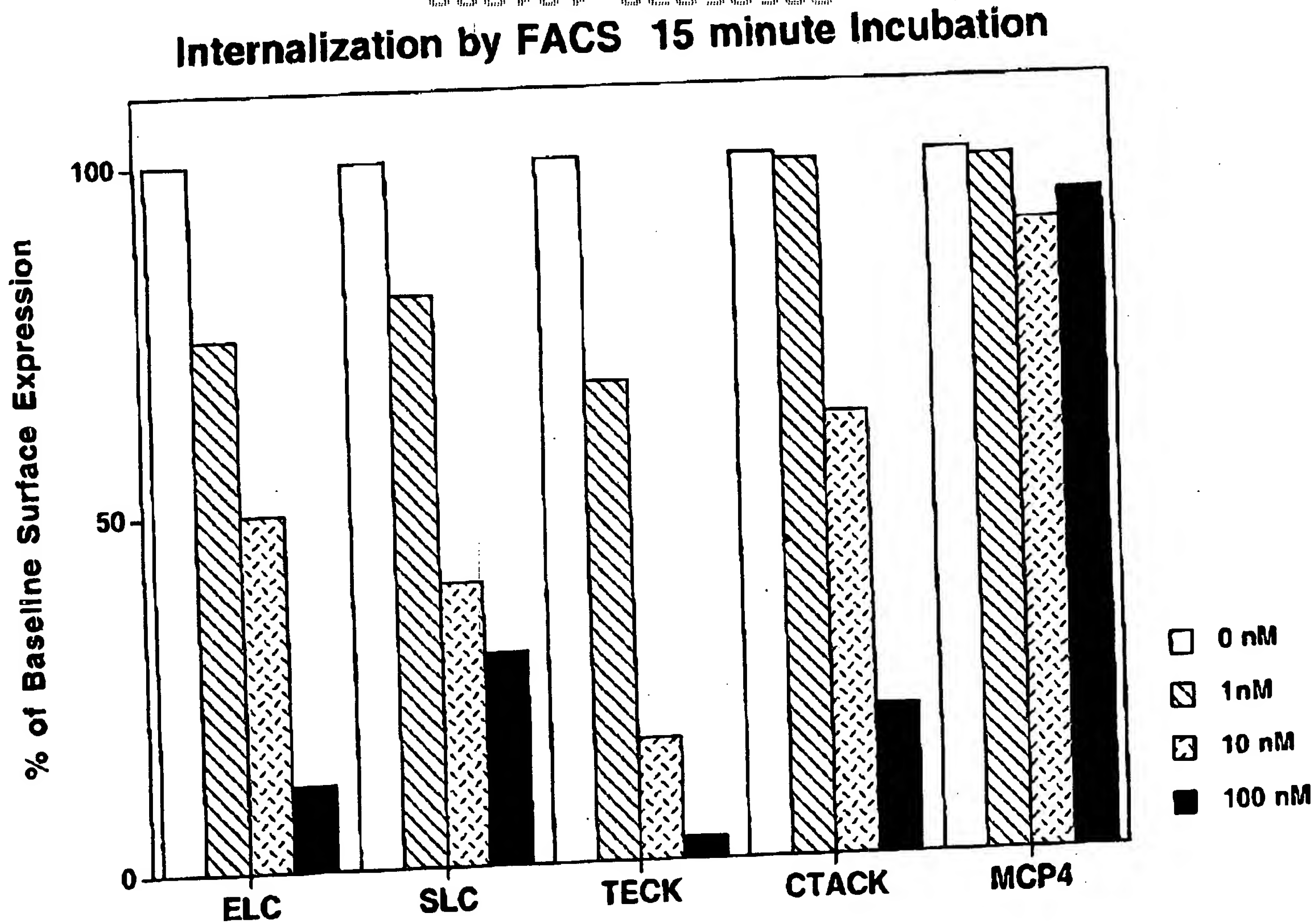


Fig. 6B